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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/709,103

DATE: 04/02/2002 (04/02
TIME: 09:33:08

Input Set : A:\60388-a-pu.txt
Output Set: N:\CRF3\04022002\I709103.raw

3 <110> APPLICANT: Cismowski, Mary
 4 Duzic, Emir
 6 <120> TITLE OF INVENTION: AGS Proteins and Nucleic Acid Molecules and Uses Therefor
 8 <130> FILE REFERENCE: 60388-A-PCT-US
 10 <140> CURRENT APPLICATION NUMBER: 09/709,103
 11 <141> CURRENT FILING DATE: 2000-11-08
 13 <160> NUMBER OF SEQ ID NOS: 73
 15 <170> SOFTWARE: PatentIn version 3.1
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 846
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Homo Sapien
 22 <220> FEATURE:
 23 <221> NAME/KEY: CDS
 24 <222> LOCATION: (1)..(843)
 25 <223> OTHER INFORMATION:
 28 <400> SEQUENCE: 1
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 33 ctg agt atc ccg gcc aag aac tgc tat ctc ccg atg gtc atc ctc ggc tcg
 34 Leu Ser Ile Pro Ala Lys Asn Cys Tyr Arg Met Val Ile Leu Gly Ser 96
 35 20 25 30
 37 tcc aag gtg ggc aag acg gcc atc gtg tgc cgc ttc ctc acc ggc cgc
 38 Ser Lys Val Gly Lys Thr Ala Ile Val Ser Arg Phe Leu Thr Gly Arg 144
 39 35 40 45
 41 ttc gag gag ccc tac acg cct acc atc gag gac ttc cac cgc aag ttc
 42 Phe Glu Asp Ala Tyr Thr Pro Thr Ile Glu Asp Phe His Arg Lys Phe 192
 43 50 55 60
 45 tac tcc atc cgc ggc gag gtc tac cag ctc gac atc ctc gac acg tcc
 46 Tyr Ser Ile Arg Gly Glu Val Tyr Gln Leu Asp Ile Leu Asp Thr Ser 240
 47 65 70 75 80
 49 ggc aac cac ccc ttc ccc gcc atg cgg cgc ctc tcc atc ctc aca gga
 50 Gly Asn His Pro Phe Pro Ala Met Arg Arg Leu Ser Ile Leu Thr Gly 288
 51 85 90 95
 53 gac gtt ttc atc ctg gtg ttc agt ctg gac aac cgc gac tcc ttc gag
 54 Asp Val Phe Ile Leu Val Phe Ser Leu Asp Asn Arg Asp Ser Phe Glu 336
 55 100 105 110
 57 gag gtg cag cgg ctc agg cag cag atc ctc gac acc aag tct tgc ctc
 58 Glu Val Gln Arg Leu Arg Gln Gln Ile Leu Asp Thr Lys Ser Cys Leu 384
 59 115 120 125
 61 aag aac aaa acc aac aag gag aac gtg gac gtg ccc ctg gtc atc tgc ggc
 62 Lys Asn Lys Thr Lys Glu Asn Val Asp Val Pro Leu Val Ile Cys Gly 432

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65	aac aag ggt gac cgc gac ttc tac cgc gag gtg gac cag cgc gag atc			480
66	Asn Lys Gly Asp Arg Asp Phe Tyr Arg Glu Val Asp Gln Arg Glu Ile			
67	145	150	155	160
69	gag cag ctg gtg ggc gac gag ccc cag cgc tgc gcc tac ttc gag atc			528
70	Glu Gln Leu Val Gly Asp Arg Pro Gln Arg Cys Ala Tyr Phe Glu Ile			
71	165	170	175	
73	tgc gcc aag aac aac agc agc ctg gac cag atg ttc cgc gcg ctc ttc			576
74	Ser Ala Lys Lys Asn Ser Leu Asp Gln Met Phe Arg Ala Leu Phe			
75	180	185	190	
77	gcc atg gcc aag ctg ccc aca gag atg agc cca gac ctg cac cgc aag			624
78	Ala Met Ala Lys Leu Pro Ser Glu Met Ser Pro Asp Leu His Arg Lys			
79	195	200	205	
81	gtc tgc gtg cag tac tgc gac gtg ctg cac aag aag ggc gct cgg aac			672
82	Val Ser Val Gln Tyr Cys Asp Val Leu His Lys Ala Leu Arg Asn			
83	210	215	220	
85	aag aag ctg ctg cgg gcc agc ggc ggc ggc ggc ggc gac ccc ggc			720
86	Lys Lys Leu Leu Arg Ala Gly Ser Gly Gly Gly Asp Pro Gly			
87	225	230	235	240
89	gac gcc ttt ggc atc gtg gca ccc ttc gcg cgc cgg ccc agc gta cac			768
90	Asp Ala Phe Gly Ile Val Ala Pro Phe Ala Arg Arg Pro Ser Val His			
91	245	250	255	
93	agc gac ctc atg tac atc cgc gag aag gcc agc gcc ggc agc cag gcc			816
94	Ser Asp Leu Met Tyr Ile Arg Glu Lys Ala Ser Ala Gly Ser Gln Ala			
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117	Ser Lys Val Gly Lys Thr Ala Ile Val Ser Arg Phe Leu Thr Gly Arg			
118	35	40	45	
121	Phe Glu Asp Ala Tyr Thr Pro Thr Ile Glu Asp Phe His Arg Lys Phe			
122	50	55	60	
125	Tyr Ser Ile Arg Gly Glu Val Tyr Gln Leu Asp Ile Leu Asp Thr Ser			
126	65	70	75	80
129	Gly Asn His Pro Phe Pro Ala Met Arg Arg Leu Ser Ile Leu Thr Gly			
130	85	90	95	
133	Asp Val Phe Ile Leu Val Phe Ser Leu Asp Asn Arg Asp Ser Phe Glu			
134	100	105	110	
137	Glu Val Gln Arg Leu Arg Gln Gln Ile Leu Asp Thr Lys Ser Cys Leu			
138	115	120	125	

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141 Lys Asn Lys Thr Lys Glu Asn Val Asp Val Pro Leu Val Ile Cys Gly	
142 130 135 140	
145 Asn Lys Gly Asp Arg Asp Phe Tyr Arg Glu Val Asp Gln Arg Glu Ile	
146 145 150 155 160	
149 Glu Gln Leu Val Gly Asp Asp Pro Gln Arg Cys Ala Tyr Phe Glu Ile	
150 165 170 175	
153 Ser Ala Lys Lys Asn Ser Ser Leu Asp Gln Met Phe Arg Ala Leu Phe	
154 180 185 190	
157 Ala Met Ala Lys Leu Pro Ser Glu Met Ser Pro Asp Leu His Arg Lys	
158 195 200 205	
161 Val Ser Val Gln Tyr Cys Asp Val Leu His Lys Lys Ala Leu Arg Asn	
162 210 215 220	
165 Lys Lys Leu Leu Arg Ala Gly Ser Gly Gly Gly Gly Asp Pro Gly	
166 225 230 235 240	
169 Asp Ala Phe Gly Ile Val Ala Pro Phe Ala Arg Arg Pro Ser Val His	
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189 <223> OTHER INFORMATION:	
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197 gccccgcgcg cgccttcgcg gcccctctgc cca atg aac ctg gcc gcg atg atc	174
198 Met Lys Leu Ala Ala Met Ile	
199 1 5	
201 aag aag atg tgc cgc agc gac tac gat ctc atc ccg gcc aag aac	
202 Lys Lys Met Cys Pro Ser Asp Ser Glu Leu Ser Ile Pro Ala Lys Asn	222
203 10 15 20	
205 tgc tat cgc atg gtc atc ctc ggc tgc tcc aag gtg ggc aag acg gcc	
206 Cys Tyr Arg Met Val Ile Leu Gly Ser Ser Lys Val Gly Lys Thr Ala	270
207 25 30 35	
209 atc gtg tgc cgc ttc ctc acc ggc cgc ttc gag gac gcc tac acg cct	
210 Ile Val Ser Arg Phe Leu Thr Gly Arg Phe Glu Asp Ala Tyr Thr Pro	318
211 40 45 50 55	
213 acc atc gag gac ttc cac cgc aag ttc tac tcc atc cgc ggc gag gtc	
214 Thr Ile Glu Asp Phe His Arg Lys Phe Tyr Ser Ile Arg Gly Glu Val	366
215 60 65 70	
217 tac cag ctc gac atc ctc gac acg ttc ggc aac cac ccg ttc ccc gcc	
218 Tyr Gln Leu Asp Ile Leu Asp Thr Ser Gly Asn His Pro Phe Pro Ala	414
219 75 80 85	

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221	atg	cg	gc	ctc	tcc	atc	ctc	aca	gga	gac	gtt	ttc	atc	ctg	gtg	ttc		462
222	Met	Arg	Arg	Leu	Ser	Ile	Leu	Thr	Gly	Asp	Val	Phe	Ile	Leu	Val	Phe		
223	90			95				100										
225	agt	ctg	gac	aac	cg	gac	tcc	tcc	gag	gag	gtg	cag	cg	ctc	agg	cag	510	
226	Ser	Leu	Asp	Asn	Arg	Asp	Ser	Phe	Glu	Glu	Val	Gln	Arg	Leu	Arg	Gln		
227	105			110				115										
229	cag	atc	ctc	gac	acc	aag	tct	tgc	ctc	aag	aac	aaa	acc	aag	gag	aac	558	
230	Gln	Ile	Leu	Asp	Thr	Lys	Ser	Cys	Leu	Lys	Asn	Lys	Thr	Lys	Glu	Asn		
231	120			125				130										
233	gtg	gac	gtg	ccc	ctg	gtc	atc	tgc	ggc	aac	aag	gg	gac	cg	gac	ttc	606	
234	Val	Asp	Val	Pro	Ile	Val	Ile	Cys	Gly	Asn	Lys	Gly	Asp	Arg	Asp	Phe		
235	140			145				150										
237	tac	cgc	gag	gtg	gac	cag	cgc	gag	atc	gag	cag	ctg	gtg	ggc	gac	gac	654	
238	Tyr	Arg	Glu	Val	Asp	Gln	Arg	Glu	Ile	Glu	Gln	Leu	Val	Gly	Asp	Asp		
239	155			160				165										
241	ccc	cag	cg	tgc	tcc	ttc	gag	atc	tcg	gcc	aag	aag	aa	gc	gc		702	
242	Pro	Gln	Arg	Cys	Ala	Tyr	Phe	Glu	Ile	Ser	Ala	Lys	Lys	Asn	Ser	Ser		
243	170			175				180										
245	ctg	gac	cag	atg	ttc	cg	cc	tcc	ttc	gcc	atg	gcc	aag	ctg	ccc	agc	750	
246	Leu	Asp	Gln	Met	Phe	Arg	Ala	Leu	Phe	Ala	Met	Ala	Lys	Leu	Pro	Ser		
247	185			190				195										
249	gag	atg	agc	cca	gac	ctg	cac	cg	cgc	aag	gtc	tcg	gtg	cag	tac	tgc	798	
250	Glu	Met	Ser	Pro	Asp	Leu	His	Arg	Lys	Val	Ser	Val	Gln	Tyr	Cys	Asp		
251	200			205				210										
253	gtg	ctg	cac	aag	aag	g	cg	ctg	cg	gg	aa	ctg	ctg	gg	cc	g	846	
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255	220			225				230										
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258	Ser	Gly	Gly	Gly	Gly	Gly	Asp	Pro	Gly	Asp	Ala	Phe	Gly	Ile	Val	Ala		
259	235			240				245										
261	ccc	tcc	g	cg	cg	ccc	agc	agc	gt	ca	agc	gac	ctc	atg	tac	atc	942	
262	Pro	Phe	Ala	Arg	Arg	Pro	Ser	Val	His	Ser	Asp	Leu	Met	Tyr	Ile	Arg		
263	250			255				260										
265	gag	aag	g	cc	g	cc	gg	cc	gg	aag	gac	aag	g	cc	tg	tc	990	
266	Glu	Lys	Ala	Ser	Ala	Gly	Ser	Gln	Ala	Lys	Asp	Lys	Glu	Arg	Cys	Val		
267	265			270				275										
269	atc	agc	tagg	cccc	cc	1046												
270	Ile	Ser																
271	280																	
273	agt	caa	atc	aa	cc	gg	cc	1106										
275	ctcc	ccgg	ccg	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	1166	
277	ctgc	ccgg	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	1226	
279	att	tgagg	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	1346	
281	ttcc	taa	aga	atc	ttt	gg	1286											
283	gtc	ttt	ccgg	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	1406	
285	gtc	tgt	ttt	ccgg	cc	1466												
287	gggg	gg	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	1526	
289	agg	aa	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	1586	
291	aaa	cc	ttt	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	1646	

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293 ttgtttttt aataataat aaaaatattt aaaatggaaa aaaaaaaaaaaa aaaaaaaaaaaa
 295 aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aagcggccgc tcgagcatgc 1706
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 301 <211> LENGTH: 281
 302 <212> TYPE: PRT
 303 <213> ORGANISM: Homo Sapien
 305 <400> SEQUENCE: 4
 307 Met Lys Leu Ala Ala Met Ile Lys Met Cys Pro Ser Asp Ser Glu
 308 1 5 10 15
 311 Leu Ser Ile Pro Ala Lys Asn Cys Tyr Arg Met Val Ile Leu Gly Ser
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 315 Ser Lys Val Gly Lys Thr Ala Ile Val Ser Arg Phe Leu Thr Gly Arg
 316 35 40 45
 319 Phe Glu Asp Ala Tyr Thr Pro Thr Ile Glu Asp Phe His Arg Lys Phe
 320 50 55 60
 323 Tyr Ser Ile Arg Gly Glu Val Tyr Gln Leu Asp Ile Leu Asp Thr Ser
 324 65 70 75 80
 327 Gly Asn His Pro Phe Pro Ala Met Arg Arg Leu Ser Ile Leu Thr Gly
 328 85 90 95
 331 Asp Val Phe Ile Leu Val Phe Ser Leu Asp Asn Arg Asp Ser Phe Glu
 332 100 105 110
 335 Glu Val Gln Arg Leu Arg Gln Gln Ile Leu Asp Thr Lys Ser Cys Leu
 336 115 120 125
 339 Lys Asn Lys Thr Lys Glu Asn Val Asp Val Pro Leu Val Ile Cys Gly
 340 130 135 140
 343 Asn Lys Gly Asp Arg Asp Phe Tyr Arg Glu Val Asp Gln Arg Glu Ile
 344 145 150 155 160
 347 Glu Gln Leu Val Gly Asp Asp Pro Gln Arg Cys Ala Tyr Phe Glu Ile
 348 165 170 175
 351 Ser Ala Lys Lys Asn Ser Ser Leu Asp Gln Met Phe Arg Ala Leu Phe
 352 180 185 190
 355 Ala Met Ala Lys Leu Pro Ser Glu Met Ser Pro Asp Leu His Arg Lys
 356 195 200 205
 359 Val Ser Val Gln Tyr Cys Asp Val Leu His Lys Ala Leu Arg Asn
 360 210 215 220
 363 Lys Lys Leu Leu Arg Ala Gly Ser Gly Gly Gly Asp Pro Gly
 364 225 230 235 240
 367 Asp Ala Phe Gly Ile Val Ala Pro Phe Ala Arg Arg Pro Ser Val His
 368 245 250 255
 371 Ser Asp Leu Met Tyr Ile Arg Glu Lys Ala Ser Ala Gly Ser Gln Ala
 372 260 265 270
 375 Lys Asp Lys Glu Arg Cys Val Ile Ser 270
 376 275 280
 379 <210> SEQ ID NO: 5
 380 <211> LENGTH: 54
 381 <212> TYPE: DNA
 382 <213> ORGANISM: Artificial Sequence
 384 <220> FEATURE:

VERIFICATION SUMMARY

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Input Set : A:\60388-a-pu.txt

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L:557 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:577 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:597 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:617 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:643 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22